

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
POLYPEPTIDE...

Okamoto, et al.

Appl. No.: Unknown

Atty Docket: TOYA136.001C1



FIG 1

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
POLYPEPTIDE...

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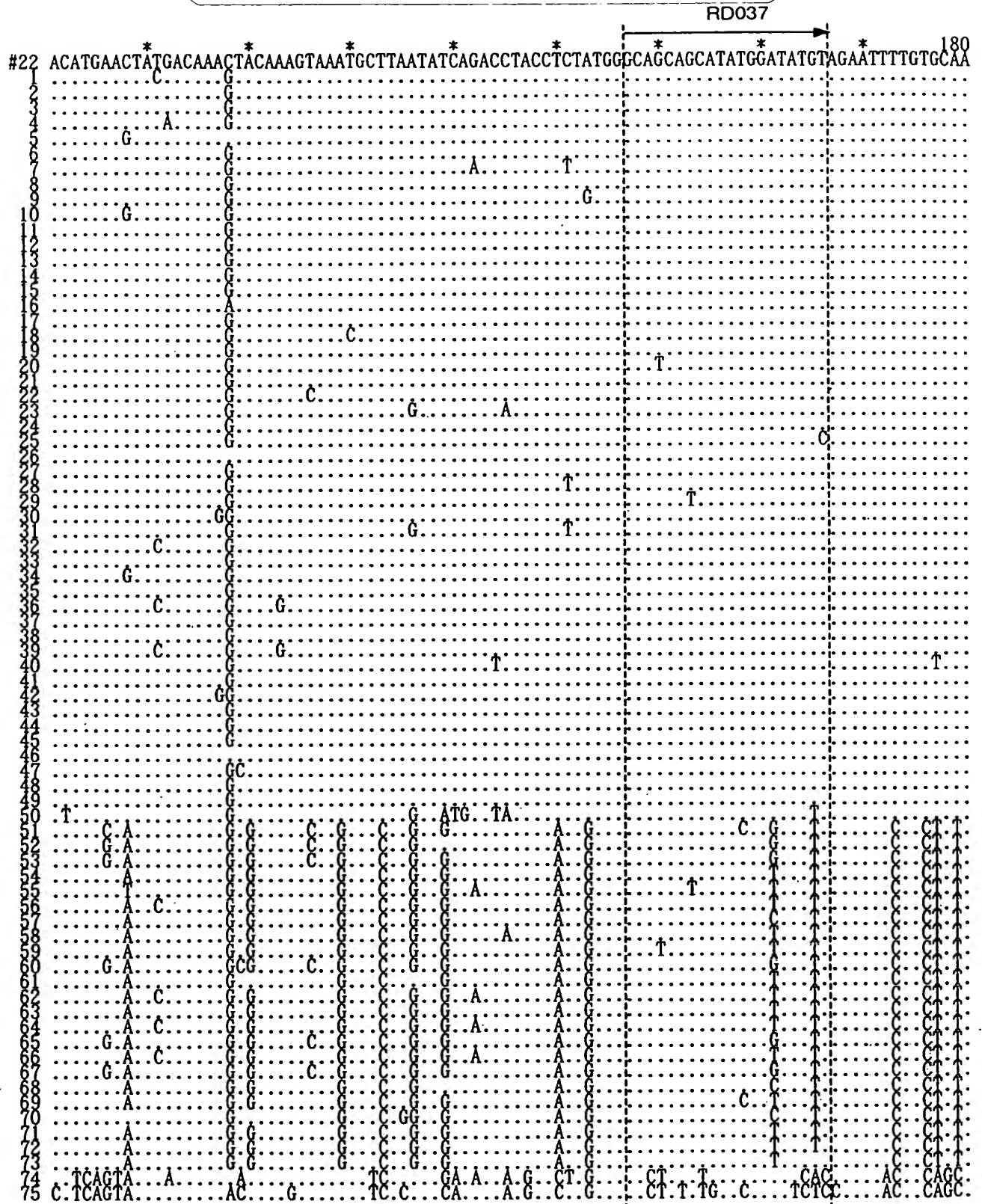


FIG 2

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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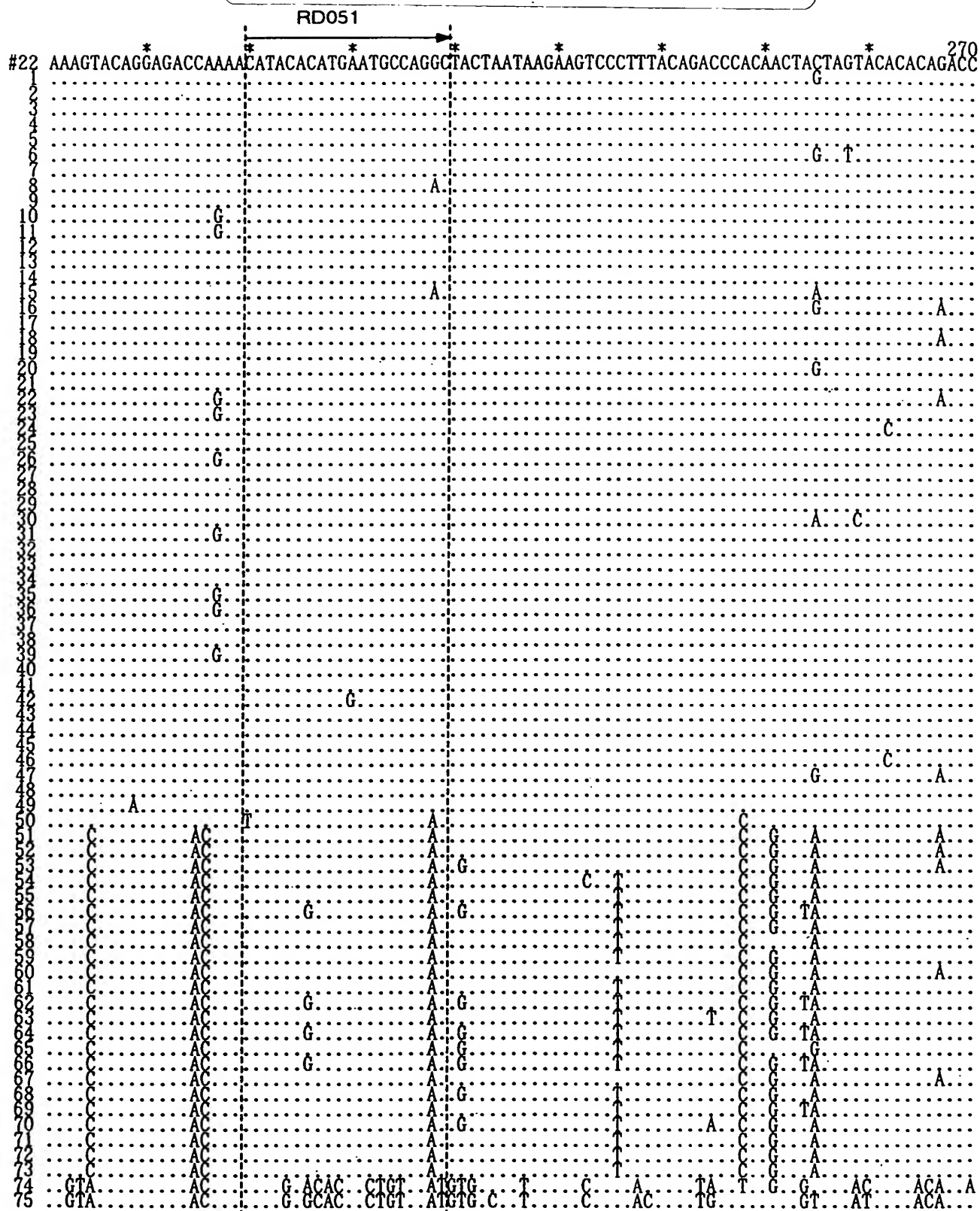


FIG 3

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#22 CCACAAAAGGCTTTGTTCCTTACTCTGTAA^{*}AAC^{*}TTTGGAATGGTAAAAATGCCAG^{*}GAGGTAGTAGTAATGTGCCTATTAGAATGAGAGC^{*}TAA^{*}
70
71
72
73
74
75

FIG 4

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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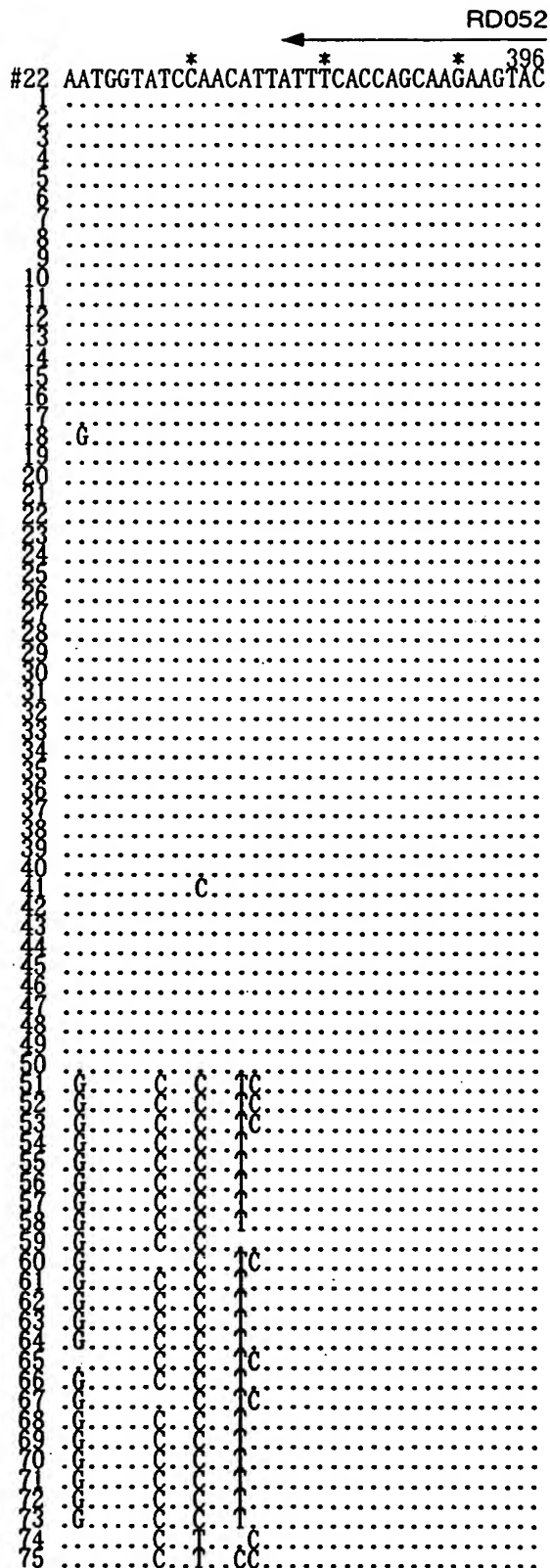


FIG 5

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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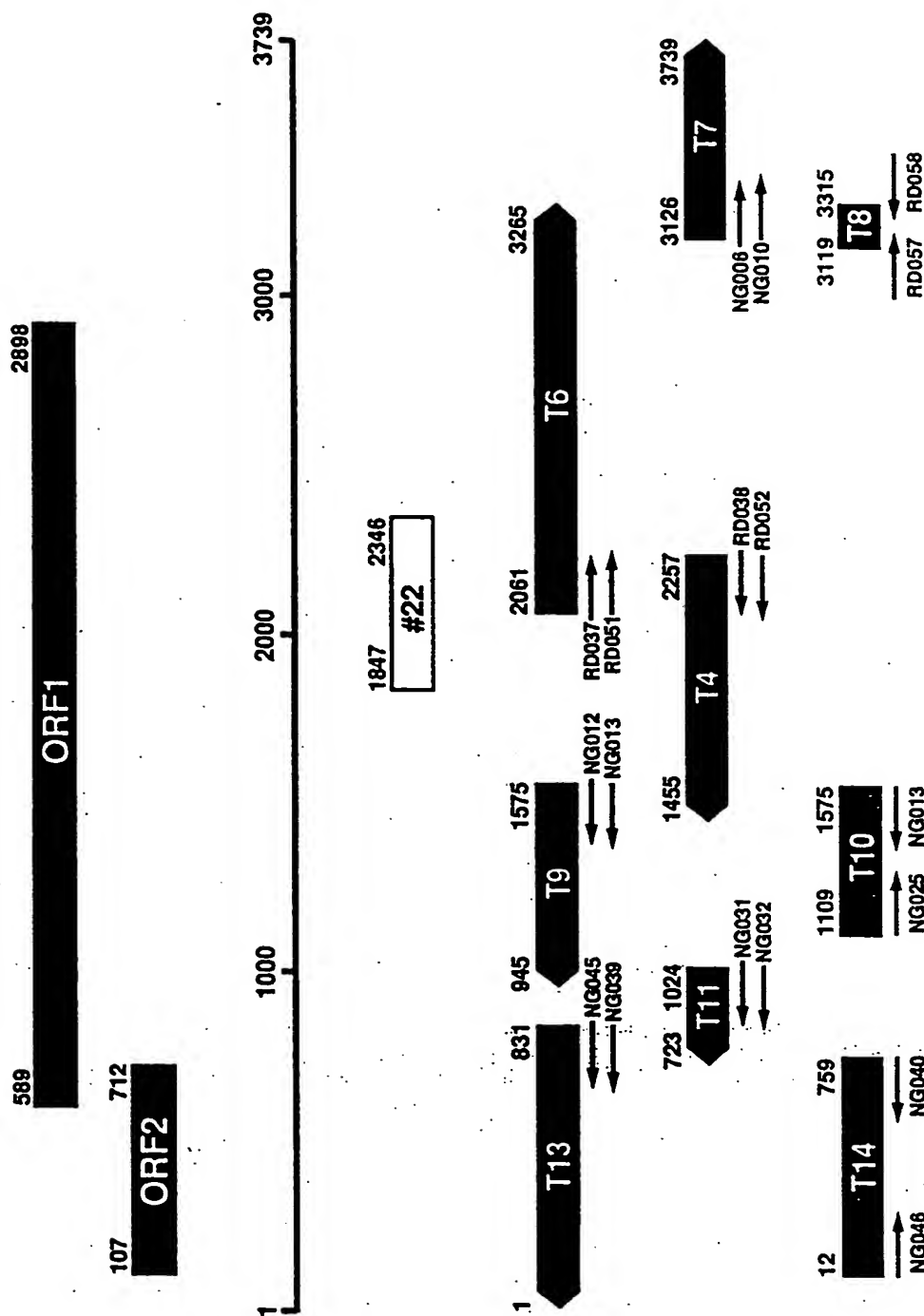


FIG 6

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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```
1) CACCAGGAGCATATACAGACATAAAGTACAATCCATTCCAGACAGAGGAGGCAACA 60
2) .....
3) .....

1) TGTTATGGATAGACTGGCTAAGCAAAAAAACAATGAACTATGACAAAGTACAAAGTAAAT 120
2) .....
3) .....

1) GCTTAATATCAGACCTACCTCTATGGCAGCAGCATATGGATATGTAGAATTTGTGCAA 180
2) .....
3) .....

1) AAAGTACAGGAGACCAGAACATACACATGAATGCCAGGCTACTAATAAGAAGTCCCTTTA 240
2) .....
3) .....

1) CAGACCCACAAC TACTAGTACACACAGACCCCAAAAGGCTTTGTCCTTACTCTTTAA 300
2) .....
3) .....

1) ACTTTGGAAATGGTAAAATGCCAGGAGGTAGTAGTAATGTGCCTATTAGAATGAGAGCTA 360
2) .....
3) .....

1) AATGGTATCCAACATTATTTCCACCAGCAAGAAGTAC 396
2) .....
3) .....
```

- 1) PILOT BLOOD FOR TRANSFUSION
- 2) PATIENT: 2 WEEKS AFTER BLOOD TRANSFUSION
- 3) PATIENT: 4 WEEKS AFTER BLOOD TRANSFUSION

FIG 7

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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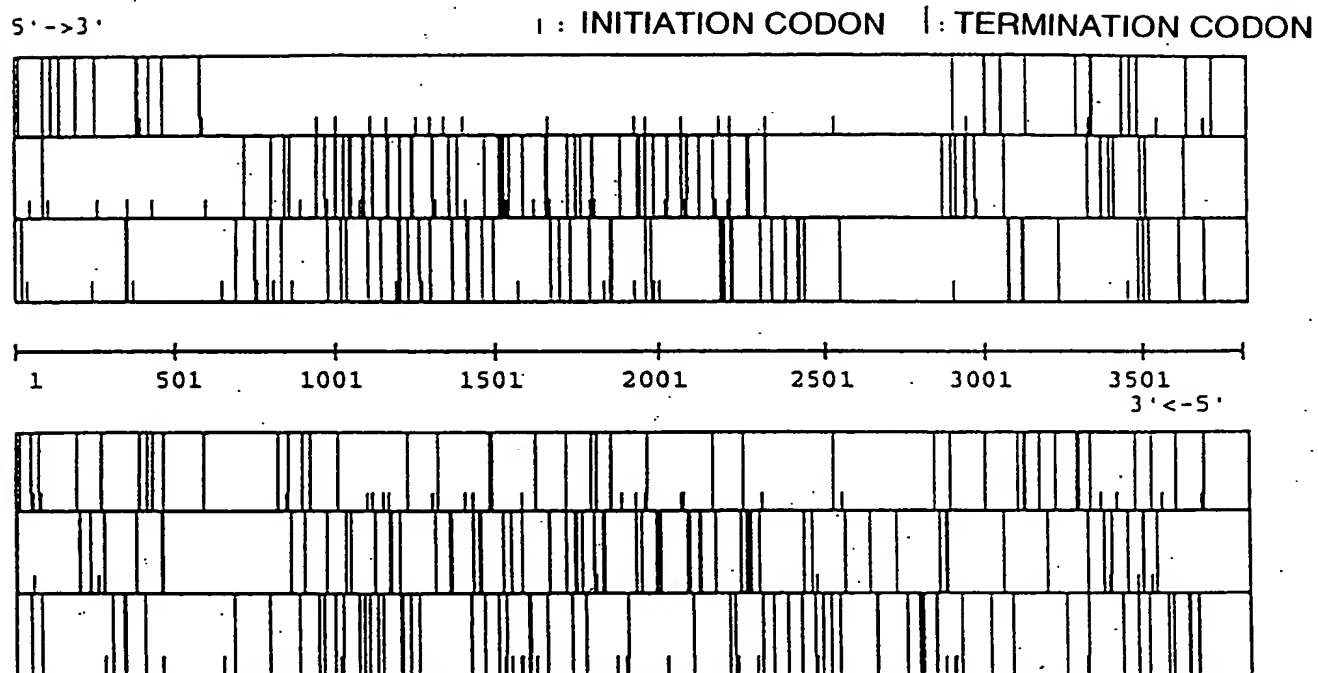


FIG 8

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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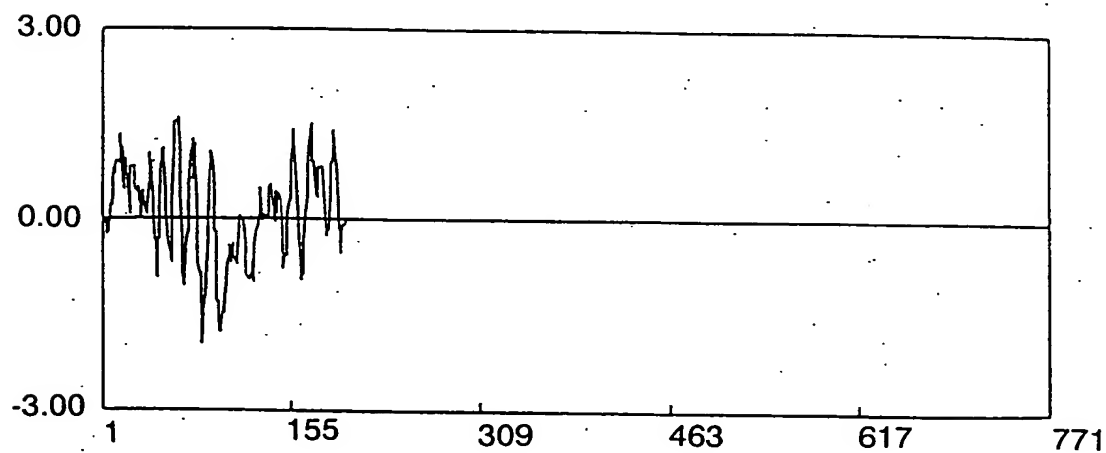
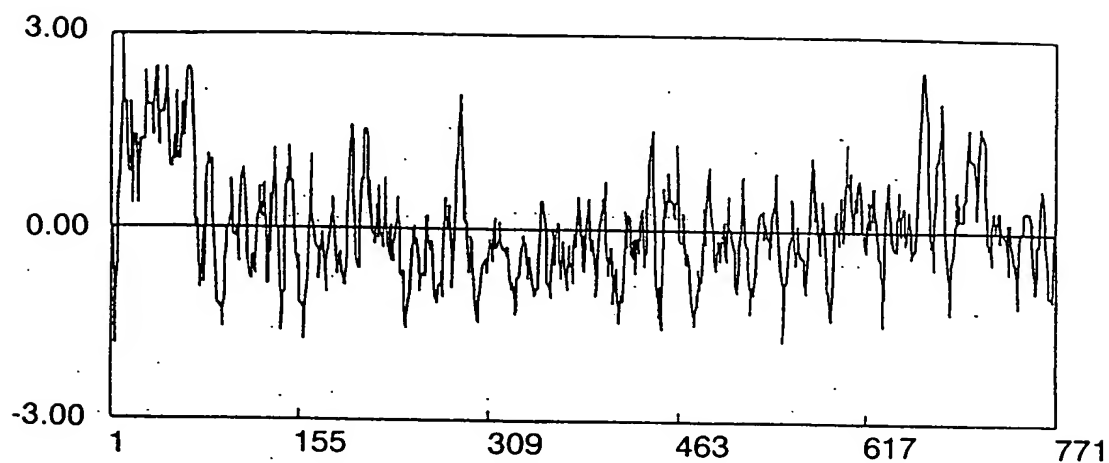


FIG 9

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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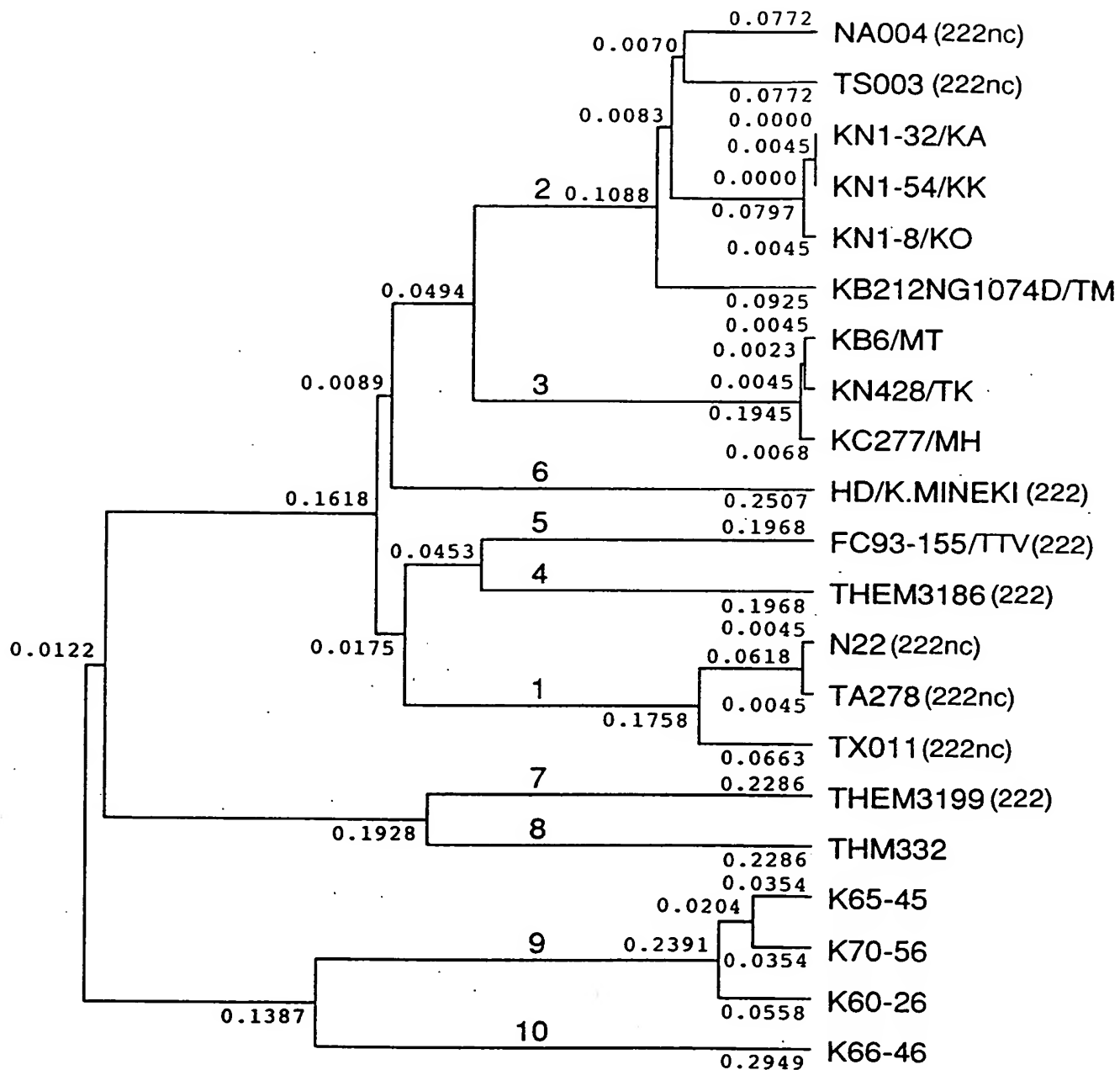


FIG 10

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FIG 11

N2Z(222nc)	1:..T.....A.....G.G.....G..C.G.G.....A.G.....	80
TA278(222nc)	1:..CT..G.TG..TCAGTA..A.....A.....TC.....GA.A..A.G..CT.G.....CT..T...	80
TX011(222nc)	1:..CT...G.T..TCAGTA.....AC..G.....TC.C..CA...A.G.C.G..CT.T.TG...	80
TS003(222nc)	1:..C...G.TG..TCAC.G..TCA..GAC..G.C.....TC.C..GAGA..T.G.....G.....CT..T...	80
NA004(222nc)	1:..C...G.TG..TCAC.G..TCA..GAC..G.C.....TC.C..GAGA..T.G.....G.....CT..T...	80
KN1-32/KA	1:..C...G.TG..TCAC.G..TCA..GAC..G.C.....TC.C..GA.A..T.G.....G.A..CT..T...	80
KN1-54/KK	1:..CT.....T.G.TCAG.A..CTCAC.GAC...C.....TC...G.T..A.G.C.....CT..TG...	80
KN1-8/KO	1:..GTA..G.C.G..TCT.GA.....GAC..GC.C.....C.T...GA.A.A.....TT..T...	80
KB212NG1074D/TM	1:..GTA..G.C.G..TCT.GA.....GAC..GC.C.....C.T...GA.A.A.....TT..T...	80
KB6/MJ	1:..GTA..G.C.G..TCT.GA.....GAC..GC.C.....C.T...GA.A.A.....TT..T...	80
KB277/MH	1:..GTA..G.C.G..TCT.GA.....GAC..GC.C.....C.T...GA.A.A.....TT..T...	80
KN428/TK	1:..TCA...TC.G..GCCCTT..CAC...GG.....C.....TGA...TT..T..C.C..C.CCT.A...	80
THEM3186(222)	1:.....TC.G.TGCAGTA..CTCTG..AA.....C.....TGCT.....TT.....CT.CTTC.T	80
FC93-155/TTV(222)	1:..G.....CC.G..GC.TA..C...CCCTCTA.G.C.....C..C.AA...T.T..C.G..TGCATG.T...	80
HD/K..MTEKI(222)	1:..TGTCCT...CG.T.C.CG.TCA..AG.CAC..C.TCC.G.CTACCG..AA...A..C.....CTGTTTCAT	80
THEM3199(222)	1:..TGC..CT.....TG...CAC.A..TCAGAG.TG..C.CCG.C.G.CT.ACC.....G.C.C..G.AC..G..CCTCT	80
THW332	1:..C.CT...CC.....CAG.G.T.....CCTG.....GT.C.....TG.....CT.....A..A.G.....C.CTTC.T	80
K65-45	1:..C.CA...CC.G..CAG.G.T.....CCTG.....GT.C.....TG.CT..GT..A..A.G.....C.CTTC.T	80
X70-56	1:..C.CT...CC.G..CAC.G.T.....CCGG.....GT.C.....G.....CT..A.T..CT.G..C.CTTT.T	80
K60-26	1:..AC.....GT.....CAG..CTCAGAG.CAG.GGC.TCT.C...C..C.GA...A.G.C.G.....CATGA.C.T	80

N22C(222nc)	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
TA278(222nc)	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
TX011(222nc)	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
TS003(222nc)	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
NA004(222nc)	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KN1-32/KK	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KN1-54/KK	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KN1-8/KO	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KB212NG1074D/TH	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KB6/MT	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KC277/WH	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
KN428/TK	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
THM3186(222)	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
F93-155/TTV(222)	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
HD/K. MINEXI(222)	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
THM3199(222)	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
THM332	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	157
K65-45	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	160
X70-56	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	160
K60-26	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	160
K66-46	81: TGGATATGTAGAAATTTTGTGCAAAAAGTACAGGAGACCAAAACATACACATGAATGCCAGGCTACTAATAAGAA//GTC	160

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FIG 12

N22(222nc)	161: CCTTTACAGACCCACAACACTACTAGTACACAGACCCACAAAGGCTTTGTCTTACTCTGTA	222
TA278(222nc)	161:	222
TX011(222nc)	161: T.....C..G..A.....T.....A..C..T...T..	222
TS003(222nc)	161: A.....TA..T..G..G...AC...ACA..AG.CTT.GG..A.AC..A..C...AGCA..	222
NA004(222nc)	161: AC...TG.....GT...AT...ACA...CTC.GG..A.AC..G..C...AG..T..T	222
KN1-32/KA	161: AC...TA.....G..GT...AC...ACA.T...CTC.G...A.AC..A..G...AGCT..T	222
KN1-54/KK	161: AC...TA.....G..GT...AC...ACA.T...CTC.G...A.AC..A..G...AGCT..T	222
KN1-8/KO	161: AC...TA.....G..GT...AC...ACA.T...CTC.G...A.AC..A..G...AGCT..T	222
KB212NG1074D/TM	161: A.....TA.....GT...AC...ACA...CTT.G...T.A.....A..TAG..T..C	222
KB6/MT	161: AC..TACA..T...A.GA...ACAC..AC...TCT..G.....A.AGTA...AGCT..T	222
KC277/MH	161: AC..TACA..T...A.GA...ACAC..AC...TCT..G.....A.AGTA...AGCT..T	222
KN428/TK	161: AC..TACA..T...A.GA...ACAC..AC...TCT..G.....A.AGTA...AGCT..T	222
THEM3186(222)	161: A.AC...T...CATG...G...AC...T..A..GA.CT.C.....A.TG...AGCAA.	222
FC93-155/TTV(222)	161: AC...G...G..G...AAC...ACA...T.TC.G..G..C..GTT.....CTAC	222
HD/K.MINEKI(222)	161: G.AC...T...T..G..TA..AA.....ACA.TGA..ACTGG.....C..C..TAGC..A.	222
THEM3199(222)	161: A.AC...A...C...GACCTCGA.AGACA...ACT..TG..A..CA..A..A..TGACTAT	222
THM332	161: A.AC...T..C.CC..CTAT.ACA.AGACA..A.AGAC.TG...ACC.A.....TGACTAC	222
K65-45	161: AC..TC.A..G.CCA.GTACAA..CTGGCA.GGTACA..CT...AC...TTC..TGACACT	225
K70-56	161: AC..TC.G...CCA.GTACAAG..CTGGCAGATACA...T...AC...TTC..TGACACT	225
K60-26	161: AC..TC.G..G.CCA.GTACAAG..CAGGCA..GTACA..T...A.....TTC..TGACACT	225
K66-46	161: T.AC..T..G..C.CCA.GTAT.ACA.G..TA.....A.AC.GT...AC..AG..A..TGACAC.	225

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NC054 (1) NT01 (795)

1-1/1-9/1-10

NC055 (692)

017-11/-12/-13

NC063 (2223)

NT04 (2094)

NC021 (3738)

NT03 (2143)

NC085 (3700)

2A-3/2B-1/2B-3

FIG 13

NON-B NON-C NON-G HEPATITIS VIRUS GENE POLYNUCLEOTIDE,
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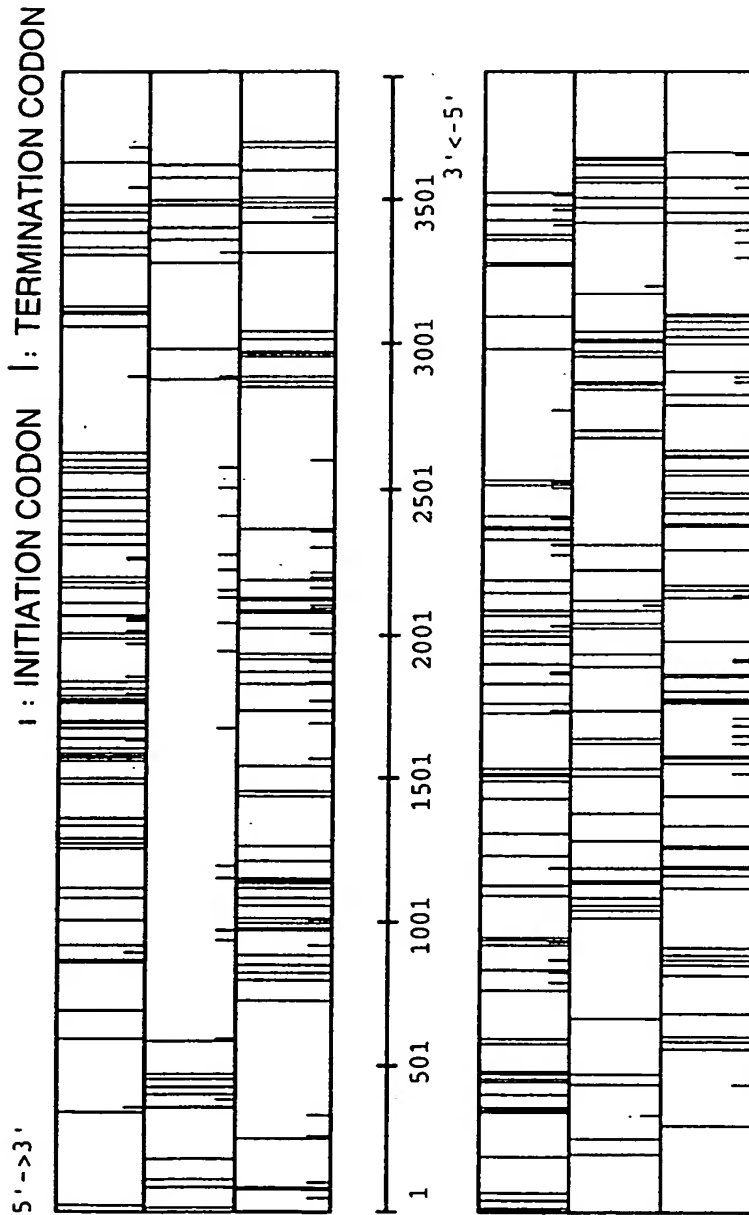


FIG 14

COMPARISON OF 5' END REGION SEQUENCES OF HNT22 (1:) AND TUS01 (2:)

1: ATTTTGCTAC	GTCACCTAAC	ACGTGACACC	CACAGGCCAA	CCGAATGCTA	TGTCAATCCAT	60
2: TTTTGCTAC	GTCACCTAAC	ACGTGACTCC	CGCAGGCCAA	CCGAGTACTA	TGTCGTCCAC	60
1: TTCCTGGGAC	GGGTCTACGT	CCTCATATAA	GTAAGTGAC	TTCCGGAATGG	CTGAGTTTTC	120
2: TTCCTGGGAC	GAGTCTACGT	CCTGATATAA	GTAAGTGAC	TTCCGGAATGG	CTGAGTTTTC	120
1: CACGCCCGTC	CGCAGCGGTC	AAAGCCACGG	AGGGAGATC	TCGCGGTCC	CGAGGCGGG	180
2: CACGCCCGTC	CGCAGCGGTC	AAAGCCACGG	AGGGAGATC	TCGCGGTCC	CGAGGCGGG	180
1: TGCCGAAGGT	GAGTTTACAC	ACCGAAGTCA	AGGGCAATT	CGGGCTCGGG	ACTGGCCGGG	240
2: TGCCGAAGGT	GAGTTTACAC	ACCGAAGTCA	AGGGCAATT	CGGGCTCGGG	ACTGGCCGGG	240
1: CTATGGGCAA	GGCTCTGAAA	AAAAGCATGT	TTATGGCAG	GCAATACAGA	AAGAAAAGGG	300
2: CCGCGGGCAA	GGCTCTTAAA	AAATGCAC	TTCGCGCAG	AGTGCAGA	GCGAAAAGGA	300

FIG 15

COMPARISON OF 3' END REGION SEQUENCES OF HNT22 (1:) AND TUS01 (2:)

1: TAA--TGA	CA TGT TTT TGG	GACCCCAAC	CTACACCC	TTCAGTAA	GACTGGAA	60
1: AGGAGTACCA	GGCCCTGTAGA	ATA TGGGACA	GACCCCTAG	AAGCAACCTA	AGAGATACCC	120
1: CCTTCTACCC	CTGGGTACCC	CAAGCAAAAC	CTAGTACCC	TGTAACTTT	AAACTTGGAT	180
1: TCAATAAAG	CTAGGCGCTG	GGAGTTTCA	TTGTCCGTGT	CTCTTCTA	AGTAACTAA	240
1: GCACTCCGAG	CGTAAGCGAG	GGTGGGACC	CTCCCTCTG	GGGCAACTCC	TTCCGAGTCC	300
1: GCGGCTACGC	GGCTTCCGCT	GGCCCGGCA	CTCAGACCC	CCCTCTCTGC	TGACACGCTC	360
1: GCGGCTTTCG	GACCACTTCC	GGTCCGGGG	GGTCCGGGAA	TTTACTAAAC	AGACTCCGAG	420
1: TTGCCATTGG	ACTCAGGAGG	TATGAATCAG	TAAACGAAGT	GAGTGGGGCC	AGACTTCCGC	480
1: ATAAAGGCCCTT	TATCTTCTTG	CCATTTGTCA	GTAAACAGGG	TCCCATAGG	CTTCCGCCCTC	540
1: CACTTTTACCT	TCTATAAAACT	ACCAAAATGG	CCGTTCAGT	GACGTCCACAG	CCGCCATTTT	600
1: AAGTAGCTGA	CGTCAAGGAT	TGACGTAAAG	GTAAAGGTG	ATCCCTCGCG	GAACTACAC	660
1: AAAATGGTGG	ACAAATCTT	CCGGGTCAA	GGTGTGCTG	ACGTCAATAAG	TCACTGGAG	720
1: GGGACCCGCT	GTAAACCGGA	AGTAGGCCCC	GTACCGTGA	TTGTCCACGTG	TGTACAAGTC	780
1: ACAACCGCCA	TTTGTGTTTA	CAAAATGGCT	GACTTCCCTTC	CTCTTTT	AAAAAAGGCG	840
1: CCAAAACAC	GTCCGGC	855				

FIG 16